

ABSTRACT

The invention provides criteria and methods for selecting optimum subsequence(s) from a target gene for targeting by a zinc finger protein. Some of the methods of target site selection seek to identify one or more target segments having a DNA motif containing one or more so-called D-able subsites having the sequence 5'NNGK3'. Other methods of the invention are directed to selection of target segments within target genes using a correspondence regime between different triplets of three bases and the three possible positions of a triplet within a nine-base site. In another aspect, the invention provides methods of designing zinc finger proteins that bind to a preselected target site. These methods can be used following the preselection of target sites according to the procedures and criteria described above. The methods of design use a database containing information about previously characterized zinc finger proteins.